

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> A nucleic acid which is upregulated in human tumor cells, a protein encoded thereby and a process for tumor diagnosis

<130> Case 20678

<140>

<141>

<150> EP00110953.7

<151> 2000-05-26

<150> EP00115369.1

<151> 2000-07-15

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 2342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (459)..(848)

<400> 1

aacctccacc acaacgctca cccttacaga cacactattg caggtctccg agggcctttg 60

ggaggccctg cttcctgcga gctgtcccgg caggacagag actcttcccg ccgcggccct 120

gccattccag gctgaggctg tgagcagcac catgacaagc tccggccgca gtggctctca 180

acagtgtggg tctctgacca cccgacgagc tggaagtgca gaccgctgac ctcccttgag 240

aacctactgg gttcttgca gtaggctctc agcgggtgtc aaacacgcc ctcagggtga 300

tctatgcacc atcacattgg aaactttttt cattgactgt tacttaatga gaagacttcc 360

ctccgggatg gttctgaagc ttccttcata ggagcaagcc tttggcggag agcactgagc 420

agacgtgcag catctttgct ggctttctacc gaaacacc atg gat cca gac gtg gtt 476

Met Asp Pro Asp Val Val

1

5

ttg tgg tcc tgc acg tgg aag cca gcc ctg cgt ggg gtg agc ctg gga 524

Leu Trp Ser Cys Thr Trp Lys Pro Ala Leu Arg Gly Val Ser Leu Gly

10

15

20

[illegible]

cagagatgaa tggcccgaaa ccctcgcgct gctctgcgcc cttcgtcatc cagtcggggt 1158
 ggtagggac tgtcagagaa aaataattta gcggccatgg ctctaactga tgtgctgcat 1218
 tctgggggtca aatgactttt acaaagtagt agtgetgcct gggtttctcta tcgtgagagc 1278
 tcagggtga taacatgaaa gaaaaaggca ctgcagccag aattcactga cattcttcac 1338
 atttcacatg agtgggacgc aggagggggg ctggggaggg tggagggatg tttcctgctt 1398
 aacagattca acagaagagt ggcaggctca gctgggtgag caaggtatcc cagcgacggg 1458
 ggacacgccc cagaccatgg gtggtggggc ttctcagagg aggtggcagg agacccgagc 1518
 ctgccaaggt tgcacctaag gtcacgggca gcattaggag ggctctctcc cagtctcccc 1578
 accccccgt cccccctccc ccaggctgca ggggtgaagt ggcttcagg acggtcactg 1638
 gcaagtttaa gctacagaga gtgtagaaac aggtgaaaa aggaagagag aggggagtaa 1698
 ataagaagga ggtgtaagaa aagaccaagc caggccccag cgccottgtg aggaagtgcc 1758
 cagggactta tgtggaagcc gtccttgctg tctgccacct tgtttttact tacattgtgt 1818
 ttttatttga gggcgagttt ggacggcaag actgatggag attgtggtct aaatgcctct 1878
 aaccactcc ttaaaatgac caccgatgt tccacaagta cttgaaaatg aatgaatggc 1938
 ttcccagagag gcagaaggca ggggtgtgcc ctacccacg ccggccaaga gttcaacaag 1998
 cattggttga caagtgaata gtgagcactt gaaccagtc acaattcaag atgagggctc 2058
 tgccatgacg catgtggtct gtgtcaccct gcagtctccc tgagcagtgt ctgaggttcg 2118
 agtgggaccc tacattcgtg aagagattta tcatctcccc aggaaaaata acagattctg 2178

tcctagggtgt tgtgatgtaa caatggtagc gatcacagcc ataacttaca attattgcat 2238
 acttacgacg agtcccgcac tgggctaagt gctttttaac tatgtgaaat gtttctttcc 2298
 ttgattgatg ccaaaatgaa taaagataat tttctgtatc tgct 2342

<210> 2

<211> 130

<212> PRT

<213> Homo sapiens

<400> 2

Met Asp Pro Asp Val Val Leu Trp Ser Cys Thr Trp Lys Pro Ala Leu
 1 5 10 15

Arg Gly Val Ser Leu Gly Leu Trp Ala Glu Asn Leu Lys His Arg Ala
 20 25 30

Gly Thr Gln Val Gln Arg Leu His Arg Pro Ser Arg Arg Arg Cys Phe
 35 40 45

Gln Ala Pro Trp Thr Asp Ser Gly Arg Ala Ala Phe Pro Pro Ser Pro
 50 55 60

Arg Gly Gly Pro Ala Leu Phe Arg Ala Trp Asp Thr Ala Gln Glu Asn
 65 70 75 80

Ala Trp Leu Val Leu Gln Thr Gln Val Leu Thr Gly Pro Ser Asp Lys
 85 90 95

Gly Gln Gly Leu Arg Leu Leu Gly Ile Ser Ala Pro Glu Pro Pro Cys
 100 105 110

Ser Gly Thr Arg Gly Leu Arg Gly Gln Glu Ala Ser Cys Val Asp Gly
 115 120 125

Gly Pro
130

<210> 3
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(285)

<400> 3
atg gat cca gac gtg gtt ttg tgg tcc tgc acg tgg aag cca gcc ctg 48
Met Asp Pro Asp Val Val Leu Trp Ser Cys Thr Trp Lys Pro Ala Leu
1 5 10 15

cgt ggg gtg agc ctg gga ctg tgg gca gag aac ctc aag cac cgg gcc 96
Arg Gly Val Ser Leu Gly Leu Trp Ala Glu Asn Leu Lys His Arg Ala
20 25 30

ggc acc caa gtg cag aga ctg cat cgt ccc aac agg agg cgc tgc ttc 144
Gly Thr Gln Val Gln Arg Leu His Arg Pro Asn Arg Arg Arg Cys Phe
35 40 45

cag gct ccc tgg acg gac tcc ggg agg gcg gcc ttt ccc ccc agc ccc 192
Gln Ala Pro Trp Thr Asp Ser Gly Arg Ala Ala Phe Pro Pro Ser Pro
50 55 60

aga ggt ggg cct gcc ctt ttc cga gcg tgg gac aca gcc cag gaa aac 240
Arg Gly Gly Pro Ala Leu Phe Arg Ala Trp Asp Thr Ala Gln Glu Asn
65 70 75 80

gca tgg ctt gtc ctc cag aca cag ggc gag ttt gga cgg caa gac 285
Ala Trp Leu Val Leu Gln Thr Gln Gly Glu Phe Gly Arg Gln Asp

85 90 95

<210> 4

<211> 95

<212> PRT

<213> Homo sapiens

<400> 4

Met Asp Pro Asp Val Val Leu Trp Ser Cys Thr Trp Lys Pro Ala Leu

1 5 10 15

Arg Gly Val Ser Leu Gly Leu Trp Ala Glu Asn Leu Lys His Arg Ala

20 25 30

Gly Thr Gln Val Gln Arg Leu His Arg Pro Asn Arg Arg Arg Cys Phe

35 40 45

Gln Ala Pro Trp Thr Asp Ser Gly Arg Ala Ala Phe Pro Pro Ser Pro

50 55 60

Arg Gly Gly Pro Ala Leu Phe Arg Ala Trp Asp Thr Ala Gln Glu Asn

65 70 75 80

Ala Trp Leu Val Leu Gln Thr Gln Gly Glu Phe Gly Arg Gln Asp

85 90 95

1364560

Sequence

<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer GSP1

<400> 5

ttatctttat tcattttgg

19

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer GSP2

<400> 6

tgcgggactc gtcgtaagta tgc

23

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer AUAP

<400> 7

ggccacgcgt cgactagtac

20

<210> 8

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer RTR-5

<400> 8

ccattcattc attttcaag

19

<210> 9

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer RTF-6

<400> 9

aaaacgcatg gcttgtc

17

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:-actin reverse
primer

<400> 10

agggtacatg gtggtgccgc cagac

25

<210> 11

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: β -actin forward
primer

<400> 11

ccaaggccaa ccgcgagaag atgac

25

<210> 12

<211> 127

<212> DNA

<213> Homo sapiens

<220>

<223> fragment of sequence AQ548392, nucleotide 1
correspond to nucleotide 304 and nucleotide 127
correspond to nucleotide 430 of the complete
sequence

<300>

<308> AQ548392

<400> 12

tggacccccg tctacacagc ttgcttcctg tccactcaga cccctggtcc cactgcatgg 60
tggctctgga gctgaaattc ctaaaagcct gagtccctgg cccttgctctg acggccctgt 120
tagcacc 127